

Listing of Claims

This listing of claims will replace all prior versions and listings of claims in the application.

1. (CURRENTLY AMENDED) A method for measuring the amount of at least two target nucleic acid sequences corresponding to at least two genes in a biological sample, comprising the steps of:
 - a) preparing a sample by combining in a sample the biological sample comprising the at least two target nucleic acid sequences corresponding to the at least two genes and a known amount of at least two standard nucleic acids, wherein said at least two standard nucleic acids have a nucleotide sequence that is one base different than the respective target nucleic acid sequence;
 - b) amplifying the sample of step a);
 - c) using a primer extension reaction at the site of differentiation to enhance a mass difference between the at least two standard nucleic acid sequences and the at least two target nucleic acid sequences corresponding to the at least two genes at the site wherein each of the standard nucleic acid sequence differs from the respective target nucleic acid sequence corresponding to the at least two genes resulting in enhanced products with different masses so that the mass differences between the at least two standard and the at least two target nucleic acid sequences corresponding to the at least two genes can be detected; and
 - d) quantifying the enhanced products of step c) by measuring the ratio of each of the amplified target nucleic acid to its corresponding amplified standard nucleic acid to measure the amount of the at least two target nucleic acid sequences corresponding to the at least two genes present in the biological sample, wherein the quantifying is performed using MALDI-TOF mass spectrometry.

2. (CURRENTLY AMENDED) The method of claim 1, wherein the at least two target nucleic acid sequences corresponding to the at least two genes are from an infectious agent.
3. (CURRENTLY AMENDED) The method of claim 1, wherein the at least two target nucleic acid sequences corresponding to the at least two genes are mRNA transcripts.
- 4.-9. (CANCELLED)
10. (CURRENTLY AMENDED) The method of claim 1, wherein one measures the amount of at least 5 target nucleic acid sequences corresponding to at least 5 genes using at least 5 respective standard nucleic acids.
11. (CURRENTLY AMENDED) The method of claim 1, wherein one measures the amount of at least 10 target nucleic acid sequences corresponding to at least 10 genes using at least 10 respective standard nucleic acids.
12. (CURRENTLY AMENDED) The method of claim 1, wherein one measures the amount of 25 target nucleic acid sequences corresponding to at least 25 genes using at least 25 respective standard nucleic acids.
13. (CURRENTLY AMENDED) The method of claim 1, wherein one measures the amount of 50 target nucleic acid sequences corresponding to at least 50 genes using at least 50 respective standard nucleic acids.
14. (CANCELLED)